GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 13, 2004, 10:22:06 ; Search time 4975 Seconds
                                        (without alignments)
                                        11257.343 Million cell updates/sec

Title: US-10-076-785A-23
Perfect score: 1369
Sequence: 1 cggcacgagtgcacctttct..........ttaaaaaaaaaaaaaaaaaa 1369

Scoring table: IDENTITY_NUC
                    Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
                    1: gb_ba:*
                    2: gb_htg:*
                    3: gb_in:*
                    4: gb_om:*
                    5: gb_ov:*
                    6: gb_pat:*
                    7: gb_ph:*
                    8: gb_pl:*
                    9: gb_pr:*
                    10: gb_ro:*
                    11: gb_sts:*
                    12: gb_sy:*
                    13: gb_un:*
                    14: gb_vi:*
                    15: em_ba:*
                    16: em_fun:*
                    17: em_hum:*
                    18: em_in:*
                    19: em_mu:*
                    20: em_om:*
                    21: em_or:*
                    22: em_ov:*
                    23: em_pat:*
                    24: em_ph:*
                    25: em_pl:*
                    26: em_ro:*
                    27: em_sts:*

```
28:   em_un:*
29:   em_vi:*
30:   em_htg_hum:*
31:   em_htg_inv:*
32:   em_htg_other:*
33:   em_htg_mus:*
34:   em_htg_pln:*
35:   em_htg_rod:*
36:   em_htg_mam:*
37:   em_htg_vrt:*
38:   em_sy:*
39:   em_htgo_hum:*
40:   em_htgo_mus:*
41:   em_htgo_other:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

<div align="center">SUMMARIES</div>

Result No.	Score	% Query Match	Length	DB	ID	Description
1	708.8	51.8	1376	8	PVZ99953	Z99953 Phaseolus v
2	705.6	51.5	1424	8	AB038598	AB038598 Vigna mun
3	608.2	44.4	1073	8	GMU71379	U71379 Glycine max
4	605	44.2	1149	8	AF138264	AF138264 Ipomoea b
5	603	44.0	1371	8	VSCYSPROT	Z30338 V.sativa mR
6	597.4	43.6	1377	8	CAR9878	AJ009878 Cicer ari
7	596	43.5	1439	8	VFU59465	U59465 Vicia faba
8	594.4	43.4	1453	8	PSCC15A	X54358 P.sativum m
9	592.2	43.3	1144	8	AF138266	AF138266 Ipomoea b
10	584.6	42.7	1143	8	AF138265	AF138265 Ipomoea b
11	578.2	42.2	1195	8	AF242373	AF242373 Ipomoea b
12	578	42.2	1310	8	AF411121	AF411121 Sanderson
13	564.4	41.2	1426	8	AF082181	AF082181 Solanum m
14	560.6	40.9	1221	8	GMU71380	U71380 Glycine max
15	558	40.8	1431	8	NTA242994	AJ242994 Nicotiana
16	551.6	40.3	1304	8	NTCYP7	Z13959 N.tabacum m
17	550	40.2	1295	8	LECYSPRO	Z14028 L.esculentu
18	528.6	38.6	1330	8	NTCYP8	Z13964 N.tabacum m
19	519	37.9	1291	8	AY039556	AY039556 Arabidops
20	519	37.9	1389	8	AY136316	AY136316 Arabidops
21	519	37.9	1398	8	BT000733	BT000733 Arabidops
22	518.8	37.9	1253	8	AF454959	AF454959 Brassica
23	517.8	37.8	1122	6	AX506629	AX506629 Sequence
24	517.8	37.8	1122	8	AY129473	AY129473 Arabidops
25	487.6	35.6	1107	6	AX412735	AX412735 Sequence
26	487.6	35.6	1107	6	AX412736	AX412736 Sequence
27	487.6	35.6	1107	6	AX506691	AX506691 Sequence
28	486.4	35.5	1249	8	AY080598	AY080598 Arabidops
29	486.4	35.5	1461	8	AY087621	AY087621 Arabidops
30	486	35.5	1138	8	AY133844	AY133844 Arabidops
31	459.4	33.6	1428	6	AR231159	AR231159 Sequence
32	447.2	32.7	1311	8	MZECP	D45402 Corn mRNA f
33	436.4	31.9	1060	8	ATTHIPRO	X74359 A.thaliana

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OM nucleic - nucleic search, using sw model

Run on:          February 13, 2004, 08:48:28 ; Search time 404 Seconds
                                             (without alignments)
                                             9147.353 Million cell updates/sec

Title:           US-10-076-785A-23
Perfect score:   1369
Sequence:        1 cggcacgagtgcacctttct..........ttaaaaaaaaaaaaaaaaaa 1369

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters:       5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       N_Geneseq_19Jun03:*
                 1:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
                 2:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
                 3:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
                 4:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
                 5:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
                 6:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
                 7:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
                 8:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
                 9:   /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
                 10:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
                 11:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
                 12:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
                 13:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
                 14:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
                 15:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
                 16:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
                 17:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
                 18:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
                 19:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
                 20:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
                 21:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
                 22:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
                 23:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
                 24:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
                 25:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
```

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1369	100.0	1369	25	ACA04869	Soybean cDNA encod
2	696.4	50.9	743	25	ACA04868 *fragment* ? (Rice) cDNA encoding
3	519	37.9	1347	21	AAC50880	Arabidopsis thalia
4	517.8	37.8	1122	24	ABZ13519	Arabidopsis thalia
5	516.6	37.7	1348	21	AAC38696	Arabidopsis thalia
6	488	35.6	1458	21	AAC47367	Arabidopsis thalia
7	487.6	35.6	1107	24	ABZ13581	Arabidopsis thalia
8	486.4	35.5	1461	21	AAC40779	Arabidopsis thalia
9	459.4	33.6	1428	22	AAF44813	Cysteine protease
10	453.6	33.1	1251	21	AAC50187	Arabidopsis thalia
11	444.4	32.5	1158	21	AAC42579	Arabidopsis thalia
12	439.6	32.1	1252	21	AAC39140	Arabidopsis thalia
13	433.6	31.7	1475	25	AAD52444	Lolium perenne LpC
14	427.2	31.2	1672	25	AAD52470	Lolium perenne CYS
15	400.8	29.3	1146	21	AAC40679	Arabidopsis thalia
16	381.2	27.8	835	22	AAF44809	Cysteine protease
17	380.2	27.8	1174	25	ACA04866	Wheat cDNA encodin
18	376	27.5	376	25	ABX20119	Human GDP-mannose
19	347	25.3	357	25	ABX20749	Human GDP-mannose
20	335.8	24.5	363	25	ABX20918	Human GDP-mannose
21	303.8	22.2	307	25	ABX20973	Human GDP-mannose
22	298	21.8	1092	21	AAC42746	Arabidopsis thalia
23	296.2	21.6	374	25	ABX19915	Human GDP-mannose
24	294.4	21.5	935	25	ACA04867	Corn cDNA encoding
25	292.4	21.4	717	25	ACA04865	Rice cDNA encoding
26	284	20.7	1134	21	AAC51518	Arabidopsis thalia
27	257.2	18.8	546	25	AAD52451	Lolium perenne DNA
28	253.2	18.5	258	25	ABX23847	Human GDP-mannose
29	250.2	18.3	758	25	AAD52449	Lolium perenne DNA
30	250.2	18.3	805	25	AAD52454	Lolium perenne DNA
31	247.8	18.1	268	25	ABX27144	Human GDP-mannose
32	247.2	18.1	789	25	AAD52448	Lolium perenne DNA
33	244.4	17.9	383	25	ABX20970	Human GDP-mannose
34	244.2	17.8	274	25	ABX25787	Human GDP-mannose
35	244	17.8	731	25	AAD52450	Lolium perenne DNA
36	239.6	17.5	573	25	ABX56910	Arabidopsis thalia
37	239	17.5	266	25	ABX33304	Human GDP-mannose
38	237.8	17.4	257	25	ABX24388	Human GDP-mannose
39	222	16.2	740	25	AAD52452	Lolium perenne DNA
40	221.6	16.2	771	25	AAD52455	Lolium perenne DNA
41	213	15.6	724	25	AAD52453	Lolium perenne DNA
42	210	15.3	797	25	AAD52456	Lolium perenne DNA
43	208.2	15.2	589	25	ABX56736	Arabidopsis thalia
44	202.2	14.8	546	21	AAC36295	Arabidopsis thalia
45	198.4	14.5	670	25	AAD52447	Lolium perenne DNA

ALIGNMENTS

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OM nucleic - nucleic search, using sw model

Run on:          February 13, 2004, 10:42:09 ; Search time 111 Seconds
                                         (without alignments)
                                         5443.725 Million cell updates/sec

Title:           US-10-076-785A-23
Perfect score:   1369
Sequence:        1 cggcacgagtgcacctttct..........ttaaaaaaaaaaaaaaaaaa 1369

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters:       1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Issued_Patents_NA:*
                 1:  /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
                 2:  /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
                 3:  /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
                 4:  /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
                 5:  /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                 6:  /cgn2_6/ptodata/2/ina/backfiles1.seq:*

         Pred. No. is the number of results predicted by chance to have a
         score greater than or equal to the score of the result being printed,
         and is derived by analysis of the total score distribution.


                              SUMMARIES
```

		% Query				
Result No.	Score	Match	Length	DB	ID	Description
1	459.4	33.6	1428	4	US-09-325-932A-118	Sequence 118, App
2	381.2	27.8	835	4	US-09-325-932A-114	Sequence 114, App
3	196.8	14.4	445	4	US-09-325-932A-116	Sequence 116, App
4	174	12.7	392	4	US-09-325-932A-125	Sequence 125, App
5	97.8	7.1	413	4	US-09-325-932A-119	Sequence 119, App
6	93.6	6.8	1463	4	US-09-325-932A-92	Sequence 92, Appl
7	88.4	6.5	1600	4	US-09-325-932A-98	Sequence 98, Appl
8	82.2	6.0	1301	2	US-08-641-314C-1	Sequence 1, Appli
9	76.4	5.6	1056	1	US-09-500-651-1	Sequence 1, Appli
10	76.4	5.6	1056	1	US-08-813-591-1	Sequence 1, Appli
11	72.6	5.3	360	4	US-09-325-932A-117	Sequence 117, App
12	72.2	5.3	1407	4	US-09-325-932A-107	Sequence 107, App

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OM nucleic - nucleic search, using sw model

Run on: February 13, 2004, 12:05:15 ; Search time 514 Seconds
                                          (without alignments)
                                          9811.076 Million cell updates/sec

Title: US-10-076-785A-23
Perfect score: 1369
Sequence: 1 cggcacgagtgcacctttct.........ttaaaaaaaaaaaaaaaaaa 1369

Scoring table: IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched: 2449703 seqs, 1841816367 residues

Total number of hits satisfying chosen parameters: 4899406

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA:*
                  1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
                  2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
                  3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
                  4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
                  5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
                  6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
                  7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
                  8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
                  9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
                  10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
                  11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
                  12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
                  13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq2:*
                  14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
                  15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
                  16: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
                  17: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
                  18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

SUMMARIES

Matches

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1369	100.0	1369	14	US-10-076-785-23 — fragment	Sequence 23, Appl
2	696.4	50.9	743	14	US-10-076-785-21	Sequence 21, Appl
3	566.6	41.4	1486	15	US-10-219-220-239	Sequence 239, App
4	517.8	37.8	1122	10	US-09-938-842A-1324	Sequence 1324, Ap
5	517.8	37.8	1122	12	US-09-938-842A-1324	Sequence 1324, Ap
6	487.6	35.6	1107	10	US-09-938-842A-1386	Sequence 1386, Ap
7	487.6	35.6	1107	12	US-09-938-842A-1386	Sequence 1386, Ap
8	459.4	33.6	1428	15	US-10-219-220-118	Sequence 118, App
9	381.2	27.8	835	15	US-10-219-220-114	Sequence 114, App
10	380.2	27.8	1174	14	US-10-076-785-17 — fragment	Sequence 17, Appl
11	(376)	27.5	376	10	US-09-878-574-2178	Sequence 2178, Ap
12	350 347	25.3	357	10	US-09-878-574-2808	Sequence 2808, Ap
13	346 335.8	24.5	363	10	US-09-878-574-2977	Sequence 2977, Ap
14	305 303.8	22.2	307	10	US-09-878-574-3032	Sequence 3032, Ap
15	322 296.2	21.6	374	10	US-09-878-574-1974	Sequence 1974, Ap
16	294.4	21.5	935	14	US-10-076-785-19	Sequence 19, Appl
17	292.4	21.4	717	14	US-10-076-785-15	Sequence 15, Appl
18	253.2	18.5	258	10	US-09-878-574-5906	Sequence 5906, Ap
19	247.8	18.1	268	10	US-09-878-574-9203	Sequence 9203, Ap
20	244.4	17.9	383	10	US-09-878-574-3029	Sequence 3029, Ap
21	244.2	17.8	274	10	US-09-878-574-7846	Sequence 7846, Ap
22	239	17.5	266	10	US-09-878-574-15363	Sequence 15363, A
23	237.8	17.4	257	10	US-09-878-574-6447	Sequence 6447, Ap
24	196.8	14.4	445	15	US-10-219-220-116	Sequence 116, App
25	181	13.2	505	14	US-10-076-785-13	Sequence 13, Appl
26	178.8	13.1	368	10	US-09-878-574-1549	Sequence 1549, Ap
27	174	12.7	392	15	US-10-219-220-125	Sequence 125, App
28	163.2	11.9	450	10	US-09-878-574-579	Sequence 579, App
29	133.2	9.7	256	10	US-09-878-574-9356	Sequence 9356, Ap
30	125.8	9.2	354	9	US-09-770-791-639	Sequence 639, App
31	116.6	8.5	253	10	US-09-878-574-8926	Sequence 8926, Ap
32	98.4	7.2	256	9	US-09-923-876-1334	Sequence 1334, Ap
33	98.4	7.2	256	12	US-09-923-876-1334	Sequence 1334, Ap
34	98	7.2	265	10	US-09-878-574-9406	Sequence 9406, Ap
35	97.8	7.1	413	15	US-10-219-220-119	Sequence 119, App
36	93.6	6.8	1463	15	US-10-219-220-92	Sequence 92, Appl
37	91.6	6.7	114	10	US-09-878-574-261	Sequence 261, App
38	91.2	6.7	296	9	US-09-294-093B-5013	Sequence 5013, Ap
39	90.2	6.6	1652	15	US-10-219-220-241	Sequence 241, App
40	88.4	6.5	1600	15	US-10-219-220-98	Sequence 98, Appl
41	78.2	5.7	1407	13	US-10-259-165-723	Sequence 723, App
42	78.2	5.7	1776	15	US-10-219-220-236	Sequence 236, App
43	78	5.7	1356	13	US-10-259-165-727	Sequence 727, App
44	76.4	5.6	1392	12	US-10-618-644-6	Sequence 6, Appli
45	76.4	5.6	1398	15	US-10-219-220-240	Sequence 240, App

ALIGNMENTS

RESULT 1
US-10-076-785-23

```
                        GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:          February 13, 2004, 10:42:05 ; Search time 2734 Seconds
                                        (without alignments)
                                        12170.017 Million cell updates/sec

Title:           US-10-076-785A-23
Perfect score:   1369
Sequence:        1 cggcacgagtgcacctttct..........ttaaaaaaaaaaaaaaaaaa 1369

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters:       45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       EST:*
                 1:   em_estba:*
                 2:   em_esthum:*
                 3:   em_estin:*
                 4:   em_estmu:*
                 5:   em_estov:*
                 6:   em_estpl:*
                 7:   em_estro:*
                 8:   em_htc:*
                 9:   gb_est1:*
                 10:  gb_est2:*
                 11:  gb_htc:*
                 12:  gb_est3:*
                 13:  gb_est4:*
                 14:  gb_est5:*
                 15:  em_estfun:*
                 16:  em_estom:*
                 17:  em_gss_hum:*
                 18:  em_gss_inv:*
                 19:  em_gss_pln:*
                 20:  em_gss_vrt:*
                 21:  em_gss_fun:*
                 22:  em_gss_mam:*
                 23:  em_gss_mus:*
                 24:  em_gss_pro:*
                 25:  em_gss_rod:*
                 26:  em_gss_phg:*
                 27:  em_gss_vrl:*
                 28:  gb_gss1:*
```

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	759.4	55.5	761	14	CA784543	CA784543 sat85c12.
	2	707.6	51.7	770	14	CA801367	CA801367 sau04g07.
c	3	699.8	51.1	732	9	AW350406	AW350406 GM210008B
	4	690.8	50.5	695	14	CA785196	CA785196 sau26a03.
c	5	664.4	48.5	773	12	BI968595	BI968595 GM830005B
c	6	638.6	46.6	657	14	CD403334	CD403334 Gm_ck2606
	7	616.4	45.0	618	13	BU763939	BU763939 sas50c05.
	8	604.4	44.1	606	13	BQ296160	BQ296160 san87d10.
	9	604.4	44.1	608	10	BF069848	BF069848 st56e09.y
	10	598.6	43.7	605	9	AW596277	AW596277 sj01d07.y
	11	589.4	43.1	668	10	BE660812	BE660812 2-D11 Gma
	12	586.6	42.8	670	10	BE660811	BE660811 0-C6 Gmax
	13	582.6	42.6	785	10	BE660817	BE660817 642 GmaxS
	14	578.4	42.2	604	13	BQ786526	BQ786526 saq69d08.
	15	577.8	42.2	581	14	CA937540	CA937540 sav20h05.
	16	572.8	41.8	576	13	BQ473664	BQ473664 sap20b10.
	17	566.8	41.4	574	10	BE555299	BE555299 sp87g09.y
	18	565.2	41.3	640	10	BE211345	BE211345 so60g02.y
	19	564.4	41.2	566	12	BI700733	BI700733 sai28e01.
	20	562.8	41.1	566	12	BI786877	BI786877 sai54d12.
	21	559.8	40.9	563	12	BM177690	BM177690 saj64d03.
	22	559.4	40.9	561	12	BM520675	BM520675 sak97b10.
	23	558.4	40.8	560	13	BQ094148	BQ094148 san42g08.
	24	558	40.8	558	9	AI794677	AI794677 sb67d05.y
c	25	549.6	40.1	648	10	BE660815	BE660815 417 GmaxS
	26	546.2	39.9	553	13	BU090659	BU090659 su07a12.y
	27	538.2	39.3	543	12	BM890906	BM890906 sam20d05.
	28	534	39.0	897	9	AI443406	AI443406 sa31g10.x
	29	525.6	38.4	590	12	BM525545	BM525545 sal29c08.
	30	523.8	38.3	539	12	BM178988	BM178988 saj61h04.
	31	522	38.1	530	12	BI972831	BI972831 sai83e12.
	32	519.6	38.0	570	13	BQ742664	BQ742664 saq54e02.
c	33	518.8	37.9	622	9	AI442849	AI442849 sa27f04.x
c	34	513.2	37.5	623	9	AI442791	AI442791 sa26e12.x
	35	512.4	37.4	571	12	BI469201	BI469201 sai08g09.
	36	509	37.2	510	13	BU081334	BU081334 sar14e03.
	37	508.8	37.2	512	12	BI468644	BI468644 sai01f05.
	38	506.6	37.0	529	12	BG791125	BG791125 sae57f08.
c	39	505	36.9	608	9	AW348222	AW348222 GM210001B
	40	503.6	36.8	519	10	BE608030	BE608030 sq19h05.y
	41	503	36.7	560	12	BM178107	BM178107 saj69b09.
	42	501.4	36.6	559	12	BI971931	BI971931 sag84c01.
	43	500.6	36.6	510	12	BG789868	BG789868 sae59a04.
	44	500	36.5	509	12	BM524944	BM524944 sal25g05.
	45	498	36.4	499	12	BG881666	BG881666 sae87c01.

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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 13, 2004, 12:53:00 ; Search time 3579 Seconds
                                          (without alignments)
                                          4183.549 Million cell updates/sec

Title: US-10-076-785A-24
Perfect score: 1966
Sequence: 1 MANLSLLFFGLLLLFSAAVAT..........NVCGVDSMVSTVAAIHVSNH 366

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext 0.5
                 Ygapop 10.0 , Ygapext 0.5
                 Fgapop 6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-
Q=/cgn2_1/USPTO_spool_p/US10076785/runat_10022004_103247_17572/app_query.fasta_1
.519
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10076785_@CGN_1_1_3745_@runat_10022004_103247_17572 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   GenEmbl:*
                 1: gb_ba:*
                 2: gb_htg:*
                 3: gb_in:*
                 4: gb_om:*
                 5: gb_ov:*
                 6: gb_pat:*
                 7: gb_ph:*
                 8: gb_pl:*
                 9: gb_pr:*
                 10: gb_ro:*

```
11:  gb_sts:*
12:  gb_sy:*
13:  gb_un:*
14:  gb_vi:*
15:  em_ba:*
16:  em_fun:*
17:  em_hum:*
18:  em_in:*
19:  em_mu:*
20:  em_om:*
21:  em_or:*
22:  em_ov:*
23:  em_pat:*
24:  em_ph:*
25:  em_pl:*
26:  em_ro:*
27:  em_sts:*
28:  em_un:*
29:  em_vi:*
30:  em_htg_hum:*
31:  em_htg_inv:*
32:  em_htg_other:*
33:  em_htg_mus:*
34:  em_htg_pln:*
35:  em_htg_rod:*
36:  em_htg_mam:*
37:  em_htg_vrt:*
38:  em_sy:*
39:  em_htgo_hum:*
40:  em_htgo_mus:*
41:  em_htgo_other:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

<div align="center">SUMMARIES</div>

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1523.5	77.5	1376	8	PVZ99953	Z99953 Phaseolus v
2	1501	76.3	1424	8	AB038598	AB038598 Vigna mun
3	1470	74.8	1149	8	AF138264	AF138264 Ipomoea b
4	1465	74.5	1144	8	AF138266	AF138266 Ipomoea b
5	1461	74.3	1143	8	AF138265	AF138265 Ipomoea b
6	1440.5	73.3	1195	8	AF242373	AF242373 Ipomoea b
7	1440	73.2	1431	8	NTA242994	AJ242994 Nicotiana
8	1435	73.0	1426	8	AF082181	AF082181 Solanum m
9	1423	72.4	1439	8	VFU59465	U59465 Vicia faba
10	1421	72.3	1377	8	CAR9878	AJ009878 Cicer ari
11	1413.5	71.9	1371	8	VSCYSPROT	Z30338 V.sativa mR
12	1413.5	71.9	1453	8	PSCC15A	X54358 P.sativum m
13	1410	71.7	1304	8	NTCYP7	Z13959 N.tabacum m
c 14	1404.5	71.4	52245	8	AP006110	AP006110 Lotus jap
15	1400	71.2	1330	8	NTCYP8	Z13964 N.tabacum m
16	1398	71.1	1107	6	AX412735	AX412735 Sequence

```
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OM protein - nucleic search, using frame_plus_p2n model

Run on:            February 13, 2004, 12:51:00 ; Search time 312 Seconds
                                              (without alignments)
                                              3166.648 Million cell updates/sec

Title:             US-10-076-785A-24
Perfect score:     1966
Sequence:          1 MANLSLLFFGLLLFSAAVAT..........NVCGVDSMVSTVAAIHVSNH 366

Scoring table:     BLOSUM62
                   Xgapop 10.0 , Xgapext  0.5
                   Ygapop 10.0 , Ygapext  0.5
                   Fgapop  6.0 , Fgapext  7.0
                   Delop   6.0 , Delext   7.0

Searched:          2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters:      5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp

Q=/cgn2_1/USPTO_spool_p/US10076785/runat_10022004_103247_17564/app_query.fasta_1
.519
-DB=N_Geneseq_19Jun03 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10076785_@CGN_1_1_396_@runat_10022004_103247_17564 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :         N_Geneseq_19Jun03:*
                   1:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
                   2:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
                   3:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
                   4:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
                   5:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
                   6:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
                   7:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
                   8:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
                   9:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
                   10:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
                   11:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
```

```
12:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
13:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
14:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
15:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
16:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
17:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
18:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
19:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
20:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
21:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
22:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
23:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
25:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1966	100.0	1369	25	ACA04869	Soybean cDNA encod
2	1398	71.1	1107	24	ABZ13581	Arabidopsis thalia
3	1398	71.1	1458	21	AAC47367	Arabidopsis thalia
4	1397.5	71.1	1122	24	ABZ13519	Arabidopsis thalia
5	1397.5	71.1	1347	21	AAC50880	Arabidopsis thalia
6	1393	70.9	1461	21	AAC40779	Arabidopsis thalia
7	1378.5	70.1	1348	21	AAC38696	Arabidopsis thalia
8	1362.5	69.3	1251	21	AAC50187	Arabidopsis thalia
9	1342.5	68.3	1158	21	AAC42579	Arabidopsis thalia
10	1332	67.8	1252	21	AAC39140	Arabidopsis thalia
11	1284.5	65.3	1672	25	AAD52470	Lolium perenne CYS
12	1282.5	65.2	1428	22	AAF44813	Cysteine protease
13	1281	65.2	1475	25	AAD52444	Lolium perenne LpC
14	1228.5	62.5	1146	21	AAC40679	Arabidopsis thalia
15	1194	60.7	743	25	ACA04868	Rice cDNA encoding
16	1113	56.6	1174	25	ACA04866	Wheat cDNA encodin
17	1071.5	54.5	1134	21	AAC51518	Arabidopsis thalia
18	1050.5	53.4	1092	21	AAC42746	Arabidopsis thalia
19	993.5	50.5	835	22	AAF44809	Cysteine protease
20	884	45.0	935	25	ACA04867	Corn cDNA encoding
21	880	44.8	717	25	ACA04865	Rice cDNA encoding
22	733	37.3	758	25	AAD52449	Lolium perenne DNA
23	727	37.0	789	25	AAD52448	Lolium perenne DNA
24	725	36.9	805	25	AAD52454	Lolium perenne DNA
25	716.5	36.4	797	25	AAD52456	Lolium perenne DNA
26	716	36.4	731	25	AAD52450	Lolium perenne DNA
27	695.5	35.4	546	25	AAD52451	Lolium perenne DNA
28	670.5	34.1	771	25	AAD52455	Lolium perenne DNA
29	667	33.9	376	25	ABX20119	Human GDP-mannose
30	645	32.8	589	25	ABX56736	Arabidopsis thalia
31	637	32.4	519	21	AAC41640	Arabidopsis thalia
32	637	32.4	1882	23	ABL04875	Drosophila melanog
33	636.5	32.4	724	25	AAD52453	Lolium perenne DNA

(handwritten annotations: "US PAP" near column heading; "Rice US2004/182704" near result 14/15)

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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 13, 2004, 14:08:25 ; Search time 85 Seconds
                                        (without alignments)
                                        1900.544 Million cell updates/sec

Title: US-10-076-785A-24
Perfect score: 1966
Sequence: 1 MANLSLLFFGLLLFSAAVAT.........NVCGVDSMVSTVAAIHVSNH 366

Scoring table: BLOSUM62
                   Xgapop 10.0 , Xgapext 0.5
                   Ygapop 10.0 , Ygapext 0.5
                   Fgapop 6.0 , Fgapext 7.0
                   Delop   6.0 , Delext   7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-
Q=/cgn2_1/USPTO_spool_p/US10076785/runat_10022004_103248_17596/app_query.fasta_1
.519
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10076785_@CGN_1_1_85_@runat_10022004_103248_17596 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Issued_Patents_NA:*
                   1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
                   2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
                   3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
                   4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
                   5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                   6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1282.5	65.2	1428	4	US-09-325-932A-118	Sequence 118, App
2	993.5	50.5	835	4	US-09-325-932A-114	Sequence 114, App
3	599.5	30.5	1642	1	US-08-723-938-2	Sequence 2, Appli
4	599.5	30.5	1642	2	US-09-080-538-2	Sequence 2, Appli
5	599.5	30.5	1642	4	US-09-387-413-2	Sequence 2, Appli
6	576	29.3	1577	3	US-08-821-994-59	Sequence 59, Appl
7	575.5	29.3	1553	3	US-08-821-994-60	Sequence 60, Appl
8	559	28.4	1463	4	US-09-325-932A-92	Sequence 92, Appl
9	544.5	27.7	1056	1	US-09-500-651-1	Sequence 1, Appli
10	544.5	27.7	1056	1	US-08-813-591-1	Sequence 1, Appli
11	544.5	27.7	1363	4	US-09-280-116-55	Sequence 55, Appl
12	542.5	27.6	1186	1	US-08-453-924-9	Sequence 9, Appli
13	537.5	27.3	2167	4	US-09-325-932A-102	Sequence 102, App
14	535.5	27.2	972	1	US-08-404-445-2	Sequence 2, Appli
15	530.5	27.0	1600	4	US-09-325-932A-98	Sequence 98, Appl
16	530	27.0	1301	2	US-08-641-314C-1	Sequence 1, Appli
17	529.5	26.9	445	4	US-09-325-932A-116	Sequence 116, App
18	521	26.5	1407	4	US-09-325-932A-107	Sequence 107, App
19	520	26.4	1643	4	US-09-701-685-1	Sequence 1, Appli
20	516	26.2	1390	3	US-08-821-994-61	Sequence 61, Appl
21	516	26.2	1441	3	US-08-821-994-63	Sequence 63, Appl
22	503	25.6	1474	4	US-09-325-932A-101	Sequence 101, App
23	502.5	25.6	1257	1	US-08-487-748A-11	Sequence 11, Appl
24	502.5	25.6	1257	3	US-08-480-070C-11	Sequence 11, Appl
25	502.5	25.6	1257	3	US-08-829-525-11	Sequence 11, Appl
26	502.5	25.6	1257	3	US-08-609-583A-11	Sequence 11, Appl
27	502.5	25.6	1257	3	US-08-937-399-11	Sequence 11, Appl
28	502.5	25.6	1257	4	US-09-310-367-11	Sequence 11, Appl
29	502.5	25.6	1257	4	US-09-032-337-11	Sequence 11, Appl
30	502.5	25.6	1257	4	US-09-464-231-11	Sequence 11, Appl
31	500	25.4	1474	3	US-08-821-994-64	Sequence 64, Appl
32	499.5	25.4	1434	3	US-08-821-994-62	Sequence 62, Appl
33	496.5	25.3	2588	4	US-09-480-017-3	Sequence 3, Appli
34	491	25.0	648	1	US-08-451-409A-3	Sequence 3, Appli
35	491	25.0	1915	3	US-09-120-365-2	Sequence 2, Appli
36	491	25.0	1915	3	US-09-515-039-2	Sequence 2, Appli
37	491	25.0	1916	3	US-09-120-365-88	Sequence 88, Appl
38	491	25.0	1916	3	US-09-515-039-88	Sequence 88, Appl
39	488	24.8	648	1	US-08-451-409A-4	Sequence 4, Appli
40	486.5	24.7	1102	3	US-08-821-994-86	Sequence 86, Appl
41	485.5	24.7	1366	3	US-08-883-526-2	Sequence 2, Appli
42	484	24.6	1839	3	US-09-120-365-4	Sequence 4, Appli
43	484	24.6	1839	3	US-09-515-039-4	Sequence 4, Appli
44	480	24.4	1661	3	US-08-821-994-82	Sequence 82, Appl
45	475.5	24.2	392	4	US-09-325-932A-125	Sequence 125, App

ALIGNMENTS

RESULT 1
US-09-325-932A-118
; Sequence 118, Application US/09325932A

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 13, 2004, 15:23:01 ; Search time 389 Seconds
                                    (without alignments)
                                    3465.834 Million cell updates/sec

Title: US-10-076-785A-24
Perfect score: 1966
Sequence: 1 MANLSLLFFGLLLFSAAVAT.........NVCGVDSMVSTVAAIHVSNH 366

Scoring table: BLOSUM62
                Xgapop 10.0 , Xgapext 0.5
                Ygapop 10.0 , Ygapext 0.5
                Fgapop 6.0 , Fgapext 7.0
                Delop   6.0 , Delext   7.0

Searched: 2449703 seqs, 1841816367 residues

Total number of hits satisfying chosen parameters: 4899406

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
—
Q=/cgn2_1/USPTO_spool_p/US10076785/runat_10022004_103250_17670/app_query.fasta_1
.519
-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10076785_@CGN_1_1_85_@runat_10022004_103250_17670
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Published_Applications_NA:*
                1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
                2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
                3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
                4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
                5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
                6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
                7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
                8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
                9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
                10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
                11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*

```
12:  /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13:  /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq2:*
14:  /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
15:  /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
16:  /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
17:  /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
18:  /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1966	100.0	1369	14	US-10-076-785-23	Sequence 23, Appl
2	1459	74.2	1486	15	US-10-219-220-239	Sequence 239, App
3	1398	71.1	1107	10	US-09-938-842A-1386	Sequence 1386, Ap
4	1398	71.1	1107	12	US-09-938-842A-1386	Sequence 1386, Ap
5	1397.5	71.1	1122	10	US-09-938-842A-1324	Sequence 1324, Ap
6	1397.5	71.1	1122	12	US-09-938-842A-1324	Sequence 1324, Ap
7	1282.5	65.2	1428	15	US-10-219-220-118	Sequence 118, App
8	1194	60.7	743	14	US-10-076-785-21	Sequence 21, Appl
9	1113	56.6	1174	14	US-10-076-785-17	Sequence 17, Appl
10	993.5	50.5	835	15	US-10-219-220-114	Sequence 114, App
11	884	45.0	935	14	US-10-076-785-19	Sequence 19, Appl
12	880	44.8	717	14	US-10-076-785-15	Sequence 15, Appl
13	667	33.9	376	10	US-09-878-574-2178	Sequence 2178, Ap
14	620.5	31.6	374	10	US-09-878-574-1974	Sequence 1974, Ap
15	603.5	30.7	1226	12	US-10-162-335-33	Sequence 33, Appl
16	601	30.6	1611	12	US-10-162-335-31	Sequence 31, Appl
17	599.5	30.5	1642	14	US-10-094-080-2	Sequence 2, Appli
18	589	30.0	2054	15	US-10-219-220-234	Sequence 234, App
19	572.5	29.1	1392	10	US-09-938-842A-1372	Sequence 1372, Ap
20	572.5	29.1	1392	12	US-09-938-842A-1372	Sequence 1372, Ap
21	571.5	29.1	505	14	US-10-076-785-13	Sequence 13, Appl
22	565	28.7	1065	12	US-10-422-555-1	Sequence 1, Appli
23	559	28.4	357	10	US-09-878-574-2808	Sequence 2808, Ap
24	559	28.4	1463	15	US-10-219-220-92	Sequence 92, Appl
25	559	28.4	1776	15	US-10-219-220-236	Sequence 236, App
26	557	28.3	1407	13	US-10-259-165-723	Sequence 723, App
27	554.5	28.2	1071	15	US-10-087-714-1	Sequence 1, Appli
28	553.5	28.2	1652	15	US-10-219-220-241	Sequence 241, App
29	553	28.1	363	10	US-09-878-574-2977	Sequence 2977, Ap
30	549.5	28.0	1392	12	US-10-618-644-6	Sequence 6, Appli
31	546	27.8	1098	12	US-10-260-238-858	Sequence 858, App
32	545.5	27.7	1590	15	US-10-219-220-235	Sequence 235, App
33	540	27.5	1308	13	US-10-259-165-441	Sequence 441, App
34	540	27.5	1311	13	US-10-259-165-107	Sequence 107, App
35	539.5	27.4	1819	15	US-10-219-220-243	Sequence 243, App
36	538.5	27.4	1374	11	US-09-784-641-3	Sequence 3, Appli
37	538.5	27.4	1374	11	US-09-784-642-3	Sequence 3, Appli
38	538.5	27.4	1374	12	US-10-462-022-3	Sequence 3, Appli
39	537.5	27.3	2167	15	US-10-219-220-102	Sequence 102, App
40	536.5	27.3	1386	12	US-10-191-803-76	Sequence 76, Appl

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 13, 2004, 13:59:35 ; Search time 2077 Seconds
                                              (without alignments)
                                              4282.830 Million cell updates/sec

Title: US-10-076-785A-24
Perfect score: 1966
Sequence: 1 MANLSLLFFGLLLFSAAVAT.........NVCGVDSMVSTVAAIHVSNH 366

Scoring table: BLOSUM62
                   Xgapop 10.0 , Xgapext 0.5
                   Ygapop 10.0 , Ygapext 0.5
                   Fgapop 6.0 , Fgapext 7.0
                   Delop   6.0 , Delext   7.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-
Q=/cgn2_1/USPTO_spool_p/US10076785/runat_10022004_103248_17584/app_query.fasta_1
.519
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10076785_@CGN_1_1_2874_@runat_10022004_103248_17584 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   EST:*
                   1: em_estba:*
                   2: em_esthum:*
                   3: em_estin:*
                   4: em_estmu:*
                   5: em_estov:*
                   6: em_estpl:*
                   7: em_estro:*
                   8: em_htc:*
                   9: gb_est1:*
                   10: gb_est2:*
                   11: gb_htc:*

```
12:    gb_est3:*
13:    gb_est4:*
14:    gb_est5:*
15:    em_estfun:*
16:    em_estom:*
17:    em_gss_hum:*
18:    em_gss_inv:*
19:    em_gss_pln:*
20:    em_gss_vrt:*
21:    em_gss_fun:*
22:    em_gss_mam:*
23:    em_gss_mus:*
24:    em_gss_pro:*
25:    em_gss_rod:*
26:    em_gss_phg:*
27:    em_gss_vrl:*
28:    gb_gss1:*
29:    gb_gss2:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1368	69.6	761	14	CA784543	CA784543 sat85c12.
	2	1315	66.9	770	14	CA801367	CA801367 sau04g07.
	3	1311.5	66.7	2610	11	AY104312	AY104312 Zea mays
	4	1231	62.6	695	14	CA785196	CA785196 sau26a03.
	5	1185.5	60.3	887	14	CD573660	CD573660 UCRPT01_0
	6	1169	59.5	741	14	CB970170	CB970170 CAB10003_
	7	1144.5	58.2	897	9	AI443406	AI443406 sa31g10.x
	8	1139.5	58.0	881	10	BF268728	BF268728 GA__Eb000
	9	1128	57.4	760	14	CB977111	CB977111 CAB40003_
	10	1121	57.0	839	14	CB894456	CB894456 EST647248
	11	1115.5	56.7	770	14	CD576271	CD576271 UCRPT01_0
	12	1115.5	56.7	808	12	BM410658	BM410658 EST584985
	13	1107.5	56.3	712	13	BQ514756	BQ514756 EST622171
	14	1107	56.3	905	14	CD574575	CD574575 UCRPT01_0
	15	1101.5	56.0	714	12	BI431639	BI431639 EST534400
c	16	1099	55.9	817	14	CB982943	CB982943 CAB70007_
	17	1095.5	55.7	820	10	BG584789	BG584789 EST486550
	18	1094	55.6	908	14	CB686321	CB686321 Bn01b_041
	19	1090	55.4	618	13	BU763939	BU763939 sas50c05.
	20	1082.5	55.1	692	14	CA909513	CA909513 PCSC18943
	21	1081.5	55.0	818	14	CB641670	CB641670 OSJNEb01G
	22	1080	54.9	606	13	BQ296160	BQ296160 san87d10.
	23	1079	54.9	888	14	CD437475	CD437475 EL01N0501
	24	1073	54.6	668	10	BE660812	BE660812 2-D11 Gma
c	25	1071.5	54.5	648	10	BE660815	BE660815 417 GmaxS
	26	1071	54.5	670	10	BE660811	BE660811 0-C6 Gmax
	27	1068	54.3	608	10	BF069848	BF069848 st56e09.y
	28	1063	54.1	795	13	BU636193	BU636193 047C01 In
	29	1062	54.0	812	14	CB291642	CB291642 UCRCS01_0